

**Figure 1**  
**Fatty Acid Biosynthetic Pathway**

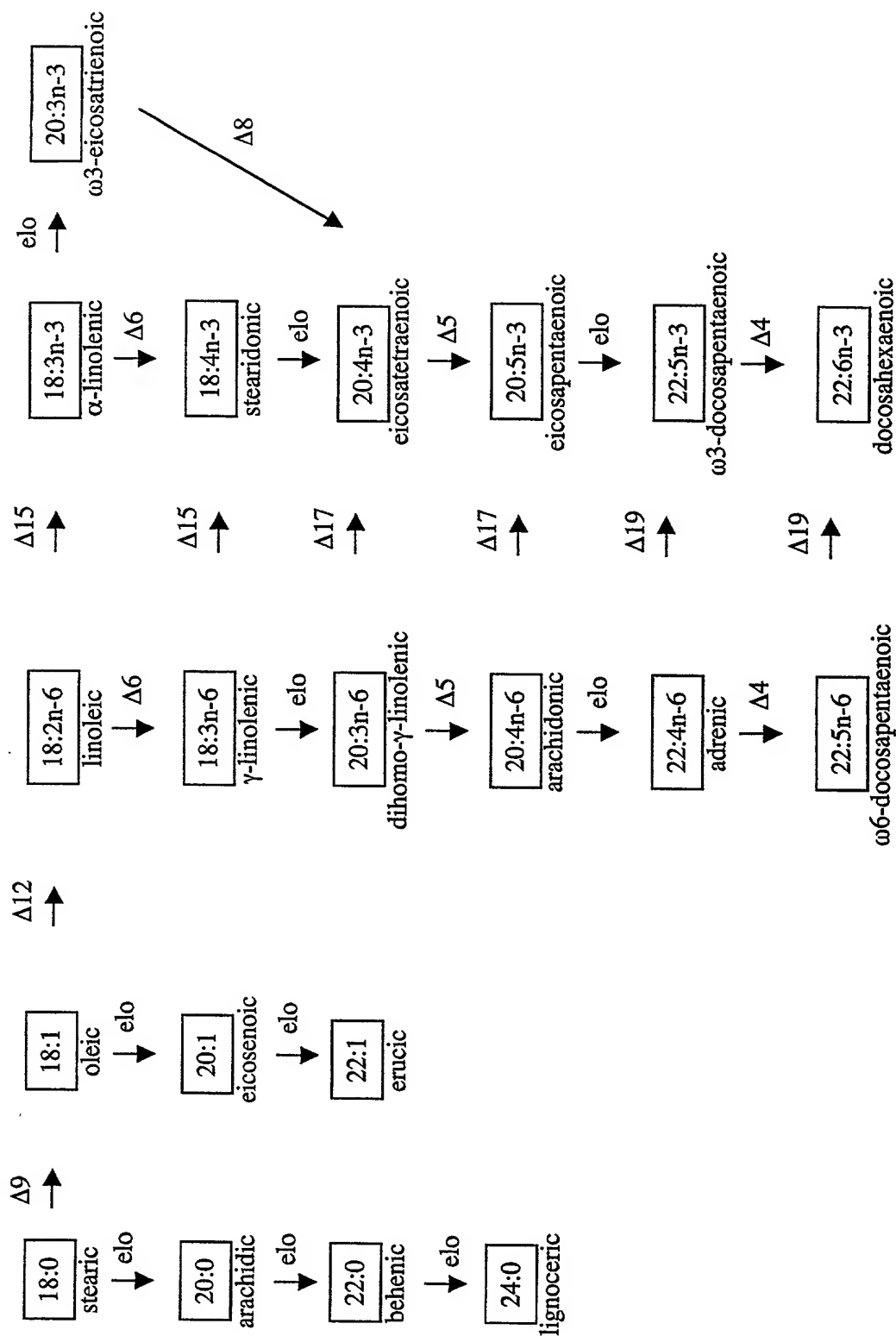


Figure 2

Gene Sequence of *sdd17*, an Omega-3 Fatty Acid Desaturase Gene  
from *Saprolegnia diclina* (ATCC 56851)

1 ATGACTGAGG ATAAGACGAA GGTCTGAGTTC CCGACGCTCA CGGAGCTCAA  
51 GCACTCGATC CCGAACGCGT GCTTTGAGTC GAACCTCGGC CTCTCGCTCT  
101 ACTACACGGC CCGCGCGATC TTCAACGCGT CGGCCTCGGC GCGCGTGCTC  
151 TACGCGGCGC GCTCGACGCC GTTCATTGCC GATAACGTTT TGCTCCACGC  
201 GCTCGTTTGC GCCACCTACA TCTACGTGCA GGGCGTCATC TTCTGGGGCT  
251 TCTTCACGGT CGGCCACGAC TCGCGGCACT CGGCCTTCTC GCGCTACCAC  
301 AGCGTCAACT TTATCATCGG CTGCATCATG CACTCTGCGA TTTTGACGCC  
351 GTTCGAGAGC TGGCGCGTGA CGCACCGCCA CCACCACAAG AACACGGGCA  
401 ACATTGATAA GGACGAGATC TTTTACCCGC ACCGGTCGGT CAAGGACCTC  
451 CAGGACGTGC GCCAATGGGT CTACACGCTC GCGCGTGCGT GGTTTGTCTA  
501 CTTGAAGGTC GGGTATGCCC CGCGCACGAT GAGCCACTTT GACCCGTGGG  
551 ACCCGCTCCT CCTTCGCCGC GCGTCGGCCG TCATCGTGTC GCTCGGCGTC  
601 TGGGCCGCCT TCTTCGCCGC GTACGCGTAC CTCACATACT CGCTCGGCTT  
651 TGCCGTCATG GGCCTCTACT ACTATGCGCC GCTCTTTGTC TTTGCTTCGT  
701 TCCTCGTCAT TACGACCTTC TTGCACCACA ACGACGAAGC GACGCCGTGG  
751 TACGGCGACT CGGAGTGGAC GTACGTCAAG GGCAACCTCT CGAGCGTCGA  
801 CCGCTCGTAC GCGCGGTTTC TGGACAACCT GAGCCACCAC ATTGGCACGC  
851 ACCAGGTCCA CCACTTGTTT CCGATCATTC CGCACTACAA GCTCAACGAA  
901 GCCACCAAGC ACTTTGCGGC CGCGTACCCG CACCTCGTGC GCAGGAACGA  
951 CGAGCCCATC ATCACGGCCT TCTTCAAGAC CGCGCACCTC TTTGTCAACT  
1001 ACGGCGCTGT GCCCGAGACG GCGCAGATCT TCACGCTCAA AGAGTCGGCC  
1051 GCGGCCGCCA AGGCCAAGTC GGACTAA

Figure 3

Amino Acid Sequence of an Omega-3 Fatty Acid Desaturase (SDD17) from *Saprolegnia diclina* (ATCC 56851)

1 MTEDKTKVEF PTLTELKHSI PNACFESNLG LSLYYTARAI FNASASAALL  
51 YAARSTPFIA DNVLLHALVC ATYIYVQGV I FWGFFTVGHD CGHSAFSRYH  
101 SVNFIIGCIM HSAILTPFES WRVTHRHHHK NTGNIDKDEI FYPHRSVKDL  
151 QDVRQWVYTL GGAWFVYLKV GYAPRTMSHF DPWDPLLLRR ASAVIVSLGV  
201 WAAFFAAYAY LTYSLGFAVM GLYYYAPLFV FASFLVITTF LHHNDEATPW  
251 YGDSEWTYVK GNLSSVDRSY GAFVDNLSSH IGTHQVHHLF PIIPHYKLNE  
301 ATKHFAAAYP HLVRRNDEPI ITAFFKTAHL FVNYGAVPET AQIFTLKESA  
351 AAKAKSD\*

Year	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

Frame: 2 initn: 733 initl: 305 opt: 689 Z-score: 996.8 expect(): 1.5e-47  
40.9% identity in 269 aa overlap  
(76-336:204-471)

	50	60	70	80	90	100
SDD17.pep	SAALLYAARSTPFTIADNVLLHALVCATYIVVQGVIFWGFFTIVGHDCGHSAFSRYHVSVNFI					
	:	:: :	:: :	:: :	:: :	:::
SYCDESB	YFFLDVGLIAGFYALAAAYLDSWFFYPFWLIQGTLFWSLVVVGHDCGHSFSKSKITLNW					
	530	560	590	620	650	680
	110	120	130	140	150	160
SDD17.pep	IGCIMHSAILTPFESWRVTIRHHHKNTIGNIDKDELFPYHRSVKDQLQ-----DVRQWVYTILG					
	: :	:  :	:  :	:  :	:  :	:  :
SYCDESB	IGHLSHTPILVPHYGWRIASHRTHHANIGNIDTDESWPVPSEQYNQMAWEKLLRFYLPL					
	710	740	770	800	830	860
	170	180	190	200	210	220
SDD17.pep	GAWFVYLKVGYAPRTMSHFDPWDPLL--RRASAVIVSLGWAAFFAAYAITYSLGFAVM					
	: :		:  :	: :  :	:  :	: :  :
SYCDESB	IAYPIYLFRRSPNRQSGSHFMGPSLFRPGEKAVALTSTFALA AFVGFLGFLTWQFGWLFL					
	890	920	950	980	1010	1040
	230	240	250	260	270	280
SDD17.pep	GLYYAPL FVFASFVL VITFLHNDEATPWYGDESWTYVKGNLSSVDRSYGA FVDNL SHH					
	:	:  :	: :	: :	: :	: :
SYCDESB	LKFYVAPYLVEFVWLDLVITFLHHTEDNLPWYRGDDWYFLKGALSTIDRDYG-FINPIIHD					
	1070	1100	1130	1160	1190	1220
	290	300	310	320	330	
SDD17.pep	IGTHQVHHLFPIIPHYKLNEATKHFAAAYPHLVRRNDEPIITAFFKT---AHLFVNYGAV					
		:  :	:  :	:  :	:  :	:  :
SYCDESB	IGTHVAHHIFSMPHYKLRRATEAKPIIGEYYRYSDEPIWAQAFKSYWACHEFVNPQSG					
	1250	1280	1310	1340	1370	1400
	340	350				
SDD17.pep	PETAQIFTLKESAAAAKAKSD					
SYCDESB	VYQSPSNGGYQKKPXLILIESNOHREGROYXMVLLPSDRLMRSMEEVKQSHSKRSALNQ					
	1430	1460	1490	1520	1550	1580

Figure 5

**Comparative analysis of *S. diclina* Delta 17-desaturase (SDD17.pep)  
*C. elegans* Delta 17-desaturase (CELEFAT)**

Frame: 1 initn: 490 init1: 222 opt: 502 Z-score: 724.0 expect(): 2.3e-32  
 31.6% identity in 310 aa overlap  
 (2-303:49-347)

				10	20	30
SDD17.pep				MTEDKTKVEFP	TLTELKHSIPNACFESNLGL	
				:: ::::    : ::::		
CELFAT	VTGGDVLVDARASLEEKEAPRDVNANTKQATTEEPRIQLPTVDAFRRAIPAHCFERDLVK	80	110	140	170	200
		40	50	60	70	80
SDD17.pep	SLYYTARAIFNASASAALLYAARSTPFIADNVLLHALVCATYIYVQGVIFWGFFTVGHDC					90
	:   :: :       :   :   :     ::   : ::::  :					
CELFAT	SIRYLVDQDF-----AALTILYFALPAFEYFGLFGYLWNIFM-----GVFGFALFVVGHDC	260	290	320	350	380
		100	110	120	130	140
SDD17.pep	GHSAFSRYHSVNFIIIGCIMHSAILTPFESWRVTHRHHHKNTGNIDKD-EIFYPHRSVKD					
	::     ::::  :       : ::::  : : :       :         :::: : : :					
CELFAT	LHGSFSDNQNLNDFIGHIAFSPLFSPIYFPWQKSHKLHHAFTNHIDKDHGHVWIQDKDWEA	410	440	470	500	530
						560
		150	160	170	180	190
SDD17.pep	LQDVRQWV-----YTLGGAWF-VYLKVGYPRTIMSHFDPWDPLILRRASAVIVSLGWAAF					200
	: : :   :: :         :       : :   : :   : :   ::					
CELFAT	MPSWKRWFNPIPFSGWLKWFVPVTLFGFC-----DGSHPYSSLFVRNSDRVQCVISGICCC	590	620	650	680	710
						740
		210	220	230	240	250
SDD17.pep	FAAYAYLTYSLGFAVMGLYYYAPLFVFASFVLVITTFLLHNDPEATPWYGDSEWTVYKGNLS					260
	: ::::    ::    : :     : :     : :   : :   : :   : : :					
CELFAT	VCAYIALTIAGSYSNWFYVWVPLSFFGLMLVIVTYLQHVDDVAEVYEADWSFVRCQTC	770	800	830	860	890
						920
		270	280	290	300	310
SDD17.pep	SVDRSYGAFVDNLSHHI-GTHQVHHLFPIIPHYKLNEATKHFAAAYPHLVRRNDEPIITA					320
	::       : :       :   :       :       :     :					
CELFAT	TIDRYYGIGLDTIMHHITDGHVAHHFFNKIPHYHLLEATEGVKKVLEPLSDTQYGYKSQV	950	980	1010	1040	1070
						1100
		330	340	350		
SDD17.pep	FFKTAHLFVNYGAVPETAQIFTLKESAAAAKAKSD					
CELFAT	NYDFFARFLWFNYKLDYLVHKTAGIMQFRITLEEKAKAKKXNIPCRSRVQQQLLRFRHFC	1130	1160	1190	1220	1250
						1280

Figure 6

Gene Sequence of *sdd12*, a Delta 12-Desaturase Gene  
from *Saprolegnia diclina* (ATCC 56851)

1 ATGTGCAAAG GTCAAGCTCC TTCCAAGGCC GACGTGTTCC ACGCTGCGGG  
51 GTACCGCCCG GTCGCCGGCA CGCCCGAGCC GCTGCCGCTG GAGCCCCCGA  
101 CGATCACGCT CAAGGACCTG CGCGCGGCGA TCCCGGCCCA CTGCTTTGAG  
151 CGCAGCGCTG CCACTAGCTT TTACCATTG GCCAAGAACC TTGCGATCTG  
201 CGCCGGCGTG TTCGCCGTTG GCCTCAAGCT CGCGGCTGCC GACTTGCCGC  
251 TCGCGGCCAA GCTGGTCGCG TGGCCCATCT ACTGGTTCGT CCAGGGCACG  
301 TACTTTACGG GCATCTGGGT CATTGCGCAC GAATGCGGCC ACCAGGCGTT  
351 CTCGGCGTCC GAGATCCTCA ACGACACGGT CGGTATCATT CTTCACTCGC  
401 TCCTCTTTGT GCCGTACCAC AGCTGGAAGA TCACGCACCG CCGCCACCAC  
451 TCCAACACGG GCAGCTGCGA GAACGACGAG GTGTTTACGC CGACGCCGCG  
501 GTCCGTCGTC GAGGCCAAGC ACGACCACTC GCTCCTCGAA GAGAGCCCGC  
551 TCTACAACCT GTACGGCATC GTCATGATGC TTCTCGTGGG CTGGATGCCG  
601 GGCTACCTCT TCTTCAACGC GACCGGCCCC ACCAAGTACG CTGGCCTCGC  
651 CAAGTCGCAC TTCAACCCGT ACGCAGCCTT TTTCTCCCA AAGGAGCGCC  
701 TCAGCATCTG GTGGAGCGAC CTCTGCTTCC TCGCGGCCTT GTACGGCTTT  
751 GGCTACGGCG TCTCGGTCTT CGGCCTCCTC GATGTCGCCC GCCACTACAT  
801 CGTGCCGTAC CTCATTGCA ACGCGTACCT CGTGCTCATC ACGTACCTCC  
851 AGCACACGGA TACGTACGTG CCCCCTTCC GCGGCGACGA GTGGAAGTGG  
901 CTGCGCGGCG CGCTCTGCAC CGTCGACCGC TCGTTCGGCG CGTGGATCGA  
951 CAGCGCGATC CACCACATTG CCGACACGCA CGTGACGCAC CACATTTTCT  
1001 CCAAGACGCC CTTCTACCAC GCGATCGAGG CGACCGACGC CATCACGCCC  
1051 CTCCTCGGCA AGTACTACCT CATCGACCCG ACGCCGATCC CGCTGGCGCT  
1101 CTGGCGCTCG TTCACGCACT GCAAGTACGT CGAGGACGAC GGCAACGTTG  
1151 TGTTTTACAA GCGCAAGCTC GAGGAAAAGT AA

Figure 7

Amino Acid Sequence of a Delta 12-Desaturase (SDD12) from *Saprolegnia diclina* (ATCC 56851)

1 MCKGQAPSKA DVFHAAGYRP VAGTPEPLPL EPPTITLKDL RAAIPAHCFE  
51 RSAATSFYHL AKNLAICAGV FAVGLKLAAA DLPLAAKLVA WPIYWVQGT  
101 YFTGIWVIAH ECGHQAFSAS EILNDTVGII LHSLLFVPYH SWKITHRRHH  
151 SNTGSCENDE VFTPTPRSVV EAKHDHSLLE ESPLYNLYGI VMMLLVGWMP  
201 GYLFFNATGP TKYAGLAKSH FNPYAAFFLP KERLSIWWSL LCFLAALYGF  
251 GYGVSFVGLL DVARHYIVPY LICNAYLVLI TYLQHTDTYV PHFRGDEWNW  
301 LRGALCTVDR SFGAWIDSAI HHIADTHVTH HIFSKTPFYH AIEATDAITP  
351 LLGKYYLIDP TPIPLALWRS FTHCKYVEDD GNVVFYKRKL EEK\*

Figure 8

**Comparative analysis of *S. diclina* Delta 12-desaturase (SDD12.pep)  
& *G. hirsutum* Delta 12-desaturase (GHO6DES)**

Frame: 3 initn: 992 initl: 413 opt: 1086 Z-score: 1531.8 expect(): 2.3e-77  
45.6% identity in 379 aa overlap  
(9-380:14-384)

SDD12.pep	MCKGQAPSKADVFAAGYRPVAGTPEP-----LPLEPPTITLKDLRAAIPAHC
GHO6DESAT	LRVSSTWRXTAFFKASKMGAGGRMPIDGIKEENRGSVNRVPIEKPPFTLGQIKQATPPHC
	10 40 70 100 130 160
SDD12.pep	FERSAATSFYHLAKNLAICAGVFAVGLKLAADLPLAAKLVAWPIYWFVQGTIFYTGIWVI
GHO6DESAT	FRRSLRLRSFSYVVHDLCLASFFYYIATSYFHF-LPQPF SYIAWPVYVWLQGCILTGWVVI
	190 220 250 280 310 340
SDD12.pep	AHECGHQAFSASEILNDIVGIIILHSLLEVPYHSWKITHRRHHSNTGSCENDEVFTPTPRS
GHO6DESAT	AHEWGHHAFRDYQWDDTVGLILHSALLVPYFSWKISHRRHHSNTGSMERDEVFVPEPKS
	370 400 430 460 490 520
SDD12.pep	VVEAKHDHSLLEESPLYNLGYVMMLLVGNMPGYLFFNATGPTKYAGLAKSHFNPYAAFF
GHO6DESAT	KLSC---FAKYLNPPGRVLSLVVITLIGW-PMYLAFNVSQ---RYYDRLASHYNPYGPIY
	550 580 610 640 670
SDD12.pep	LPKERLSIWSDLCFLAALYGFYGVSVFGLLDVARHYIVPYLICNAYLVLTITLQHTDT
GHO6DESAT	SDRERLQVYISDTGIFAVIYVLYKIAATKGLAWLLCTYGVPLLVNAFLVLITLQHTHS
	700 730 760 790 820 850
SDD12.pep	YVPHFRGDEWNWLRGALCTVDRSFGAWIDSAIHIIADTHVTHHIFSKTPFYHATEATDAI
GHO6DESAT	ALPHYDSSEWDWLRGALSTMDRDFGV-LNKVFHNTIDTHVAHHLFSTMPHYHAMEATKAI
	880 910 940 970 1000 1030
SDD12.pep	TPILGKYLLIDPTPIPLALWRSFTHCKYVEDDGNVVFYKRKLEEK
GHO6DESAT	KPILGKYYPFDGTPIYKAMWREAKECLYVEPDVGGGGGSGKGVFWYRNKFXRPTNCLTAG
	1060 1090 1120 1150 1180 1210
GHO6DESAT	RRNQKTYLLDXCLGKLIINGRKMWNLSCLVVLCTKCCINKLYGRKKKK
	1240 1270 1300 1330 1360

20070926 10:00:00



**Figure 9**

**Sequence ID:**

Sequence ID 1

5' -ATC CGC GCC GCC ATC CCC AAG CAC TGC TGG GTC AAG-3'

Sequence ID 2

5' - GCC CTC TTC GTC CTC GGC CAY GAC TGC GGC CAY GGC TCG TTC TCG-  
3'

Sequence ID 3

5' -GAG RTG GTA RTG GGG GAT CTG GGG GAA GAR RTG RTG GRY GAC RTG-3'

Sequence ID 4

5' -CCC TAC CAY GGC TGG CGC ATC TCG CAY CGC ACC CAY CAY CAG AAC-3'

Sequence ID 5

5' -GTT CTG RTG RTG GGT CCG RTG CGA GAT GCG CCA GCC RTG GTA GGG-3'

Sequence ID 6

5' - GGC TCG CAC TTC SAC CCC KAC TCG GAC CTC TTC GTC-3'

Sequence ID 7

5' - GAC GAA GAG GTC CGA GTM GGG GTW GAA GTG CGA GCC-3'

Sequence ID 8

5' - GCG CTG GAK GGT GGT GAG GCC GCC GCG GAW GSA CGA CCA-3'

Sequence ID 9

5' - CTG GGG GAA GAG RTG RTG GAT GAC RTG GGT GCC GAT GTC RTG RTG-  
3'

Sequence ID 10

5' - GGT GGC CTC GAY GAG RTG GTA RTG GGG GAT CTK GGG GAA GAR RTG-  
3'

Sequence ID 11

5' -GAG RTG GTA RTG GGG GAT CTG GGG GAA GAR RTG RTG GRY GAC RTG-3'

Sequence ID 12

5' -TAC GCG TAC CTC ACG TAC TCG CTC G-3'

Sequence ID 13

5' -TTC TTG CAC CAC AAC GAC GAA GCG ACG-3'

Sequence ID 14

5' -GGA GTG GAC GTA CGT CAA GGG CAA C-3'

Sequence ID 15

5' -TCA AGG GCA ACC TCT CGA GCG TCG AC-3'

Sequence ID 16

5' -CCC AGT CAC GAC GTT GTA AAA CGA CGG CCA G-3'

Sequence ID 17

5' - AGC GGA TAA CAA TTT CAC ACA GGA AAC AGC -3'

Sequence ID 18

5' -GGT AAA AGA TCT CGT CCT TGT CGA TGT TGC-3'

Sequence ID 19

5' -GTC AAA GTG GCT CAT CGT GC-3'

Sequence ID 20

5' -CGA GCG AGT ACG TGA GGT ACG CGT AC-3'

Sequence ID 21

5' -TCA ACA GAA TTC ATG ACC GAG GAT AAG ACG AAG GTC GAG TTC CCG-3'

Sequence ID 22

5'-AAA AGA AAG CTT CGC TTC CTA GTC TTA GTC CGA CTT GGC CTT GGC-3'

Sequence ID 23

5'-TCA ACA AAG CTT ATG ACC GAG GAT AAG ACG AAG GTC GAG TTC  
CCG-3'

Sequence ID 24

5'-AAA AGA GAA TTC CGC TTC CTA GTC TTA GTC CGA CTT GGC CTT  
GGC-3'

Sequence ID 25

1 ATGACTGAGG ATAAGACGAA GGTCGAGTTC CCGACGCTCA CGGAGCTCAA  
51 GCACTCGATC CCGAACGCGT GCTTTGAGTC GAACCTCGGC CTCTCGCTCT  
101 ACTACACGGC CCGCGCGATC TTCAACGCGT CGGCCTCGGC GGCGCTGCTC  
151 TACGCGGCGC GCTCGACGCC GTTCATTGCC GATAACGTTC TGCTCCACGC  
201 GCTCGTTTGC GCCACCTACA TCTACGTGCA GGGCGTCATC TTCTGGGGCT  
251 TCTTCACGGT CGGCCACGAC TGCGGCCACT CGGCCTTCTC GCGCTACCAC  
301 AGCGTCAACT TTATCATCGG CTGCATCATG CACTCTGCGA TTTTGACGCC  
351 GTTCGAGAGC TGGCGCGTGA CGCACCGCCA CCACCACAAG AACACGGGCA  
401 ACATTGATAA GGACGAGATC TTTTACCCGC ACCGGTCGGT CAAGGACCTC  
451 CAGGACGTGC GCCAATGGGT CTACACGCTC GGCGGTGCGT GGTTTGTCTA  
501 CTTGAAGGTC GGGTATGCCC CGCGCACGAT GAGCCACTTT GACCCGTGGG  
551 ACCCGCTCCT CCTTCGCCGC GCGTCGGCCG TCATCGTGTC GCTCGGCGTC  
601 TGGGCCGCCT TCTTCGCCGC GTACGCGTAC CTCACATACT CGCTCGGCTT  
651 TGCCGTCATG GGCCTCTACT ACTATGCGCC GCTCTTTGTC TTTGCTTCGT  
701 TCCTCGTCAT TACGACCTTC TTGCACCACA ACGACGAAGC GACGCCGTGG  
751 TACGGCGACT CGGAGTGGAC GTACGTCAAG GGCAACCTCT CGAGCGTCGA  
801 CCGCTCGTAC GGC GCGTTTCG TGGACAACCT GAGCCACCAC ATTGGCACGC  
851 ACCAGGTCCA CCACTTGTTT CCGATCATTC CGCACTACAA GCTCAACGAA  
901 GCCACCAAGC ACTTTGCGGC CGCGTACCCG CACCTCGTGC GCAGGAACGA  
951 CGAGCCCATC ATCACGGCCT TCTTCAAGAC CGCGCACCTC TTTGTCAACT  
1001 ACGGCGCTGT GCCCCGAGACG GCGCAGATCT TCACGCTCAA AGAGTCGGCC  
1051 GCGGCCGCCA AGGCCAAGTC GGA CTAA

Sequence ID 26

1 MTEDKTKVEF PTLTELKHSI PNACFESNLG LSLYYTARAI FNASASAALL  
 51 YAARSTPFIA DNVLLHALVC ATYIYVQGVI FWGFFTVDGHD CGHSAFSRYH  
 101 SVNFIIGCIM HSAILTPFES WRVTHRHHHK NTGNIDKDEI FYPHRSVKDL  
 151 QDVRQWVYTL GGAWFVYLKV GYAPRTMSHF DPWDPLLLRR ASAVIVSLGV  
 201 WAAFFAAYAY LTYSLGFAVM GLYYYAPLFV FASFLVITTF LHHNDEATPW  
 251 YGDSEWTVYVK GNLSSVDRSY GAFVDNLSSH IGTHQVHHLF PIIPHYKLNE  
 301 ATKHFAAAYP HLVRNDEPI ITAFFKTAHL FVNYGAVPET AQIFTLKESA  
 351 AAKAKSD\*

Sequence ID 27

1 ATGGCCCCGC AGACGGAGCT CCGCCAGCGC CACGCCGCCG TCGCCGAGAC  
 51 GCCGGTGGCC GGCAAGAAGG CCTTTACATG GCAGGAGGTC GCGCAGCACA  
 101 ACACGGCGGC CTCGGCCTGG ATCATTATCC GCGGCAAGGT CTACGACGTG  
 151 ACCGAGTGGG CCAACAAGCA CCCC GGCGGC CGCGAGATGG TGCTGCTGCA  
 201 CGCCGGTCGC GAGGCCACCG ACACGTTCGA CTCGTACCAC CCGTTCAGCG  
 251 ACAAGGCCGA GTCGATCTTG AACAAGTATG AGATTGGCAC GTTCACGGGC  
 301 CCGTCCGAGT TTCCGACCTT CAAGCCGGAC ACGGGCTTCT ACAAGGAGTG  
 351 CCGCAAGCGC GTTGGCGAGT ACTTCAAGAA GAACAACCTC CATCCGCAGG  
 401 ACGGCTTCCC GGGCCTCTGG CGCATGATGG TCGTGTTTGC GGTCGCCGGC  
 451 CTCGCCTTGT ACGGCATGCA CTTTTCGACT ATCTTTGCGC TGCAGCTCGC  
 501 GGCCGCGGCG CTCTTTGGCG TCTGCCAGGC GCTGCCGCTG CTCCACGTCA  
 551 TGCACGACTC GTCGCACGCG TCGTACACCA ACATGCCGTT CTTCCATTAC  
 601 GTCGTGCGCC GCTTTGCCAT GGAAGTGGTTT GCCGGCGGCT CGATGGTGTC  
 651 ATGGCTCAAC CAGCACGTCG TGGGCCACCA CATCTACACG AACGTCGCGG  
 701 GCTCGGACCC GGATCTTCCG GTCAACATGG ACGGCGACAT CCGCCGCATC  
 751 GTGAACCGCC AGGTGTTCCA GCCCATGTAC GCATTCCAGC ACATCTACCT  
 801 TCCGCCGCTC TATGGCGTGC TTGGCCTCAA GTTCCGCATC CAGGACTTCA  
 851 CCGACACGTT CGGCTCGCAC ACGAACGGCC CGATCCGCGT CAACCCGCAC  
 901 GCGCTCTCGA CGTGGATGGC CATGATCAGC TCCAAGTCGT TCTGGGCCTT  
 951 CTACCGCGTG TACCTTCCGC TTGCCGTGCT CCAGATGCCC ATCAAGACGT  
 1001 ACCTTGCGAT CTTCTTCCTC GCCGAGTTTG TCACGGGCTG GTACCTCGCG  
 1051 TTCAACTTCC AAGTAAGCCA TGTCTCGACC GAGTGCGGCT ACCCATGCGG  
 1101 CGACGAGGCC AAGATGGCGC TCCAGGACGA GTGGGCAGTC TCGCAGGTCA

1151 AGACGTCGGT CGACTACGCC CATGGCTCGT GGATGACGAC GTTCCTTGCC  
 1201 GGCGCGCTCA ACTACCAGGT CGTGCACCAC TTGTTCCCA GCGTGTGCGA  
 1251 GTACCACTAC CCGGCGATCG CGCCCATCAT CGTCGACGTC TGCAAGGAGT  
 1301 ACAACATCAA GTACGCCATC TTGCCGGACT TTACGGCGGC GTTCGTTGCC  
 1351 CACTTGAAGC ACCTCCGCAA CATGGGCCAG CAGGGCATCG CCGCCACGAT  
 1401 CCACATGGGC TAA

Sequence ID 28

1 ATGGCAAACA GCAGCGTGTG GGATGATGTG GTGGGCCGCG TGGAGACCGG  
 51 CGTGGACCAG TGGATGGATG GCGCCAAGCC GTACGCACTC ACCGATGGGC  
 101 TCCCGATGAT GGACGTGTCC ACCATGCTGG CATTTCGAGGT GGGATACATG  
 151 GCCATGCTGC TCTTCGGCAT CCCGATCATG AAGCAGATGG AGAAGCCTTT  
 201 TGAGCTCAAG ACCATCAAGC TCTTGACAAA CTTGTTTCTC TTCGGACTTT  
 251 CCTTGATCAT GTGCGTGGAG ACCATCCGCC AGGCTATCCT CGGAGGCTAC  
 301 AAAGTGTTTG GAAACGACAT GGAGAAGGGC AACGAGTCTC ATGCTCAGGG  
 351 CATGTCTCGC ATCGTGTACG TGTTCTGCGT GTCCAAGGCA TACGAGTTCT  
 401 TGGATACCGC CATCATGATC CTTTGCAAGA AGTTCAACCA GGTTTCCTTC  
 451 TTGCATGTGT ACCACCATGC CACCATTTTT GCCATCTGGT GGGCTATCGC  
 501 CAAGTACGCT CCAGGAGGTG ATGCGTACTT TTCAGTGATC CTCAACTCTT  
 551 TCGTGCACAC CGTCATGTAC GCATACTACT TCTTCTCCTC CCAAGGGTTC  
 601 GGGTTTCGTGA AGCCAATCAA GCCGTACATC ACCACCCTTC AGATGACCCA  
 651 GTTCATGGCA ATGCTTGTGC AGTCCTTGTA CGACTACCTC TTCCCATGCG  
 701 ACTACCCACA GGCTCTTGTG CAGCTTCTTG GAGTGTACAT GATCACCTTG  
 751 CTTGCCCTCT TCGGCAACTT TTTTGTGCAG AGCTATCTTA AAAAGCCAAA  
 801 AAAGAGCAAG ACCAACTAA

Sequence ID 29

1 MTVGFDFTVT MDTVRNHNMP DDAWCAIHGT VYDITKFSKV HPGGDIIMLA  
 51 AGKEATILFE TYHIKGVDA VLRKYKVGKL PQGKKGETSH MPTGLDSASY  
 101 YSWDSEFYRV LRERVAKKLA EPGLMQRRM ELWAKAIFLL AGFWGSLYAM  
 151 CVLDPHGGAM VAAVTLGVFA AFVGTCTIQHD GSHGAFSKSR FMNKAAGWTL  
 201 DMIGASAMTW EMQHVLGHP YTNLIEMENG LAKVKGADVD PKKVDQESDP  
 251 DVFSTYPMLR LHPWHRQRFY HKFQHLIAPL IFGFMTINKV ISQDVGVLRL  
 301 KRLFQIDANC RYGSPWNVAR FWIMKLLTTL YMVALPMMQ GPAQGLKLF

351 MAHFTCGEVL ATMFIVNHII EGVSYASKDA VKGVMAPPRT VHGVTPMQVT  
401 QKALSAAEST KSDADKTTMI PLNDWAAVQC QTSVNWAVGS WFWNHFSGGL  
451 NHQIEHHCFP QNPHTVNVYI SGIVKETCEE YGVPYQAEIS LFSAYFKMLS  
501 HLRTLGNEDL TAWST\*

Sequence ID 30

5'-CCG SAG TTC ACS ATC AAG GAG ATC CGC GAS KSC ATC CCG GCC  
CAC TGC TTC -3'

Sequence ID 31

5'-GRS CTT CTT GAK GTG GWM SGT GGC CTC CTC GGC GTG GTA GWR  
CGG CAT-3'

Sequence ID 32

5'-CCS STC TAC TGG GCC TGC CAG GGT RTC GTC CTC ACS GGT GTC  
TGG-3'

Sequence ID 33

5'-CCS STC TAC TGG ATC RYS CAG GGT RTC GTC KGY ACS GGT GTC  
TGG-3'

Sequence ID 34

5'-GGC GTG GTA GTG CGG CAT SMM CGA GAA GAR GTG GTG GGC GAC  
GTG-3'

Sequence ID 35

5'-CAC GTA CCT CCA GCA CAC GGA CAC CTA CG-3'

Sequence ID 36

5'- GAT CGA CAG CGC GAT CCA CCA CAT TGC-3'

Sequence ID 37

5'- CAA ATG GTA AAA GCT AGT GGC AGC GCT GC-3'

Sequence ID 38

5'-AGT ACG TGC CCT GGA CGA ACC AGT AGA TG-3'

Sequence ID 39

5' - TCA ACA GAA TTC ATG TGC AAA GGT CAA GCT CCT TCC AAG GCC  
GAC GTG -3'

Sequence ID 40

5' - AAA AGA AAG CTT TTA CTT TTC CTC GAG CTT GCG CTT GTA AAA  
CAC AAC-3'

Sequence ID 41

1 ATGTGCAAAG GTCAAGCTCC TTCCAAGGCC GACGTGTTCC ACGCTGCGGG  
51 GTACCGCCCCG GTCGCCGGCA CGCCGAGCC GCTGCCGCTG GAGCCCCCGA  
101 CGATCACGCT CAAGGACCTG CGCGCGGCGA TCCCGGCCCA CTGCTTTGAG  
151 CGCAGCGCTG CCACTAGCTT TTACCATTG GCCAAGAACC TTGCGATCTG  
201 CGCCGGCGTG TTCGCCGTTG GCCTCAAGCT CGCGGCTGCC GACTTGCCGC  
251 TCGCGGCCAA GCTGGTCGCG TGGCCCATCT ACTGGTTCGT CCAGGGCACG  
301 TACTTTACGG GCATCTGGGT CATTGCGCAC GAATGCGGCC ACCAGGCGTT  
351 CTCGGCGTCC GAGATCCTCA ACGACACGGT CGGTATCATT CTTCACTCGC  
401 TCCTCTTTGT GCCGTACCAC AGCTGGAAGA TCACGCACCG CCGCCACCAC  
451 TCCAACACGG GCAGCTGCGA GAACGACGAG GTGTTTACGC CGACGCCGCG  
501 GTCCGTGCTC GAGGCCAAGC ACGACCACTC GCTCCTCGAA GAGAGCCCGC  
551 TCTACAACCT GTACGGCATC GTCATGATGC TTCTCGTGGG CTGGATGCCG  
601 GGCTACCTCT TCTTCAACGC GACCGGCCCG ACCAAGTACG CTGGCCTCGC  
651 CAAGTCGCAC TTCAACCCGT ACGCAGCCTT TTTCTCCCA AAGGAGCGCC  
701 TCAGCATCTG GTGGAGCGAC CTCTGCTTCC TCGCGGCCTT GTACGGCTTT  
751 GGCTACGGCG TCTCGGTCTT CGGCCTCCTC GATGTCGCCC GCCACTACAT  
801 CGTGCCGTAC CTCATTTGCA ACGCGTACCT CGTGCTCATC ACGTACCTCC  
851 AGCACACGGA TACGTACGTG CCCCACTTCC GCGGCGACGA GTGGAAGTGG  
901 CTGCGCGGCG CGCTCTGCAC CGTCGACCGC TCGTTCGGCG CGTGGATCGA  
951 CAGCGCGATC CACCACATTG CCGACACGCA CGTGACGCAC CACATTTTCT  
1001 CCAAGACGCC CTTCTACCAC GCGATCGAGG CGACCGACGC CATCACGCCC  
1051 CTCCTCGGCA AGTACTACCT CATCGACCCG ACGCCGATCC CGCTGGCGCT  
1101 CTGGCGCTCG TTCACGCACT GCAAGTACGT CGAGGACGAC GGCAACGTTG

1151 TGTTTTACAA GCGCAAGCTC GAGGAAAAGT AA

Sequence ID 42

1 MCKGQAPSKA DVFHAAGYRP VAGTPEPLPL EPPTITLKDL RAAIPAHCFE  
51 RSAATSFYHL AKNLAICAGV FAVGLKLAAA DLPLAAKLVA WPIYWVQGT  
101 YFTGIWVIAH ECGHQAFSAS EILNDTVGII LHSLLFVPYH SWKITHRRHH  
151 SNTGSCENDE VFTPTPRSVV EAKHDHSLLE ESPLYNLYGI VMMLLVGWMP  
201 GYLFFNATGP TKYAGLAKSH FNPYAAFFLP KERLSIWWSL LCFLAALYGF  
251 GYGVSVFGLL DVARHYIVPY LICNAYLVLI TYLQHTDTYV PHFRGDEWNW  
301 LRGALECTVDR SFGAWIDSAI HHIADTHVTH HIFSKTPFYH AIEATDAITP  
351 LLGKYYLIDP TPIPLALWRS FTHCKYVEDD GNVVIFYKRKL EEK\*